

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Zsebo, Krisztina M.  
Bosselman, Robert A.  
Suggs, Sidney V.  
Martin, Francis H.
- (ii) TITLE OF INVENTION: Stem Cell Factor: Composition Claims
- (iii) NUMBER OF SEQUENCES: 104
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
  - (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
  - (C) CITY: Chicago
  - (D) STATE: Illinois
  - (E) COUNTRY: United States of America
  - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 09/005,893
  - (B) FILING DATE: 12-JAN-1998
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/449,653
  - (B) FILING DATE: 24-MAY-1995
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 07/982,255
  - (B) FILING DATE: 25-NOV-1992
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 07/589,701
  - (B) FILING DATE: 01-OCT-1990
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 07/573,616
  - (B) FILING DATE: 24-AUG-1990

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/537,198
- (B) FILING DATE: 11-JUN-1990

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/422,383
- (B) FILING DATE: 16-OCT-1989

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Clough, David W.
- (B) REGISTRATION NUMBER: 36,107
- (C) REFERENCE/DOCKET NUMBER: 01017/35136

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 312/474-6300
- (B) TELEFAX: 312/474-0448
- (C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Glu	Glu	Ile	Cys	Arg	Asn	Pro	Val	Thr	Asp	Asn	Val	Lys	Asp	Ile	Thr
1				5					10					15	
Lys	Leu	Val	Ala	Asn	Leu	Pro	Asn	Asp	Tyr	Met	Ile	Thr	Leu	Asn	Tyr
			20					25					30		
Val	Ala	Gly	Met	Asp	Val	Leu	Pro	Ser	His	Cys	Trp	Leu	Arg	Asp	Met
		35					40					45			
Val	Thr	His	Leu	Ser	Val	Ser	Leu	Thr	Thr	Leu	Leu	Asp	Lys	Phe	Ser
	50					55					60				
Asn	Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Gly
65				70					75					80	
Lys	Ile	Val	Asp	Asp	Leu	Val	Ala	Cys	Met	Glu	Glu	Asn	Ala	Pro	Lys
			85					90					95		
Asn	Val	Lys	Glu	Ser	Leu	Lys	Lys	Pro	Glu	Thr	Arg	Asn	Phe	Thr	Pro
		100					105						110		
Glu	Glu	Phe	Phe	Ser	Ile	Phe	Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp
		115					120					125			

Phe Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Ser Thr Leu  
130 135 140  
Gly Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu  
145 150 155 160  
Pro Pro Val Ala Ala  
165

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /mod\_base= Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACRTTYTTNG GNGCRTTYTC YTCCAT

26

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 12 and 15
- (D) OTHER INFORMATION: /mod\_base= Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AARAAATCYT CNGGNGTRAA RTT

23

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTATCNGGYT TYTT

14

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGARGARA AYCCCCCAA RAAYGT

26

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCNAAYGAYT AYATGWTMAC

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGNGGNARCA TRAANGGYTT

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACCAKAAARAT CTTYAAAANCG ATC

23

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTATTTTCAA TAGATCCATT GA

22

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAACTATGT CGCC

14

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTAGTCAAGC TGACTGATAA G

21

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TAACCAACAA TGACTAGGCA A

21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTCCAGAGTC AGTGTC

16

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGAAGCTTG CCTTTCCTTA TGAAGAAGA

29

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGCCGCGGT TACGGTGGTA ACATGAAGGG CTTTGTGA

38

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATAAATGCA AGTGATAATC C

21

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCGGTCGACC CGCGGAACTT TAAGTCCATG CAACAC

36

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CACCCGCGGT TATGCAACAG GGGGTAACAT AAATGG

36

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CACCCGCGGT TAGGCTGCAA CAGGGGGTAA CATAAA

36

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

18

CTTAATGTTG AAGAAACC

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

22

GATGGTAGTA CAATTGTCAG AC

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

22

GTCTGACAAT TGTACTACCA TC

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

22

CAATTTAGTG ACGTCTTTTA CA

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTAGATGAGT TTTCTTTCAC GCAC

24

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAATCATTCA AGAGCCCAGA ACCC

24

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACATCCATC CCGGGGAC

18

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTGGCAATAT TTTAAGTCTC AAGAAGACC

29

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCGCCGCGGC TCCTATAGGT GCTAATTGG

29

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCTCACCCT GTTTGTGCTG GATCGCA

27

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGTGTCTAGA CTTGTGTCTT CTCATAAGG A

31

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCCCCCHGG

10

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTT TTTTTTTTGG

20

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTTTTTTTTT TTTTTTTTAG

20

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTTTTTTTTT TTTTTTTTCG

20

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTCGCGCGAT CAGGCCCCCC CCCC

24

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCGGCCGGA TAGGCCTTTT TTTTTTTTTT

30

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGCCGGATAG GCCTCACNNN NNNT

24

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGCCGGATAG GCCTCAC

17

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4673 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(660..773, 1184..1246, 2053..2223, 2837..2993, 3692..3774)

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: join(720..773, 1184..1246, 2053..2223, 2837..2993, 3692..3774)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AAAGTATCTT TCTATTGGCG AAGGACATGT TTTCCCATAA GTGGTAAACA AACTGTCTGC	60
ACATAATAAT TATCTTGCTG CCGTAAAGAT TAGGTAAAT TCTGCCTTCG ATCTAAAAAC	120
ACACCCTTCT GTCAATCCGA GGAGCAGTGT GCTAGTCTAG AGGTCTAAAT GAAGGCTCCT	180
TTCACGGTTG TATTTCTGCT CCCCAAATTG TCCACATTTA AAAGGAGAGT GCTTCTTTTC	240
AGCCTTAGGC TCTGAATTTT ATGCATTTCCT CCATTTTCCG AGGTCCCCC CAAGTGATAA	300
TTCTGTTACA CGTTGCTACA AGTTCATCCC TAATTGCCGT CAAGAACTG ACTGTAGAAG	360
GCTTACCACA GACGTTGTAA CCGACAGTAA AGCCATTGAA AGAGTAATTC AAACAGGATG	420
GAAGCCAGCA GTATTTTGTG GCTGTTGCTC TTTTCTTTT CAGTTTGGTG AGAGCAGCTT	480
GAATGCTTAA CATTAAAGCC ATCAGCTTAA AACAAAACAA AACAAAACAA AAAAAACCC	540
CGCTCTGGCA TATTTGCACT TAACACATAC GGTATAAGGT GTTACTGGTT TGCATAGTTC	600
TGGATTTTTT TTTTTTAAAA ACTGATGGAC ACCAAGAAAT GTTCTGTTC TTTGTTAG	659
ACT TGG ATT ATC ACT TGC ATT TAT CTT CAA CTG CTC CTA TTT AAT CCT	707
Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro	
-20 -15 -10 -5	
CTC GTC AAA ACT CAG GAG ATC TGC AGG AAT CCT GTG ACT GAT AAT GTA	755
Leu Val Lys Thr Gln Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val	
1 5 10	
AAA GAC ATT ACA AAA CTG GTAAGTAAAG AATGATTTTG GCATCTATAA	803
Lys Asp Ile Thr Lys Leu	
15	
GTCTTCCCTG TGCTTGCTGA CCACATAGGT TCAGGGCACT CCCGACAGGA GTTCCCAGCT	863
TTCTAAGATA AGGAATCACT GTACGAGTCT GAAGTGCTTC TTCTGGGCAA ATGGGAGATG	923
CTTAGGTCAT GGAGGGTTTA TCTGTATAAC TGGCCCTTTG CACACCAACA AAGTGACTGA	983
CTGGCTTTTG CCTGTTACCT ACTGTCTCCA GTCCTGGGCA TGGTATATAC TTAGGCACCC	1043
AAGATTGGAT TTACAACTCA AGCATTATAT ATTGGACAAC ACGGGGTATG AGATATTAAT	1103
GATATGTCAG GTTGGATGGA TGAGTTTCT CAAGAAATTC TCTTGATTTT ACTCACGTTT	1163
TCATTTCTTG GTCTCTGTAG GTG GCG AAT CTT CCA AAT GAC TAT ATG ATA	1213
Val Ala Asn Leu Pro Asn Asp Tyr Met Ile	
20 25	
ACC CTC AAC TAT GTC GCC GGG ATG GAT GTT TTG GSTATGTAGTC CACACACTTC	1266
Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu	
30 35	
TGAGTTGCCT TTTAGTAGCT AATGGGTGAC CTGTGCTTAT TCACATTGAA GACATTATTT	1326

GCTCTTTGTC GTTTTTAGAT GTTGACCTAT AATTTTTCCT TCAAGCTGCT GCTAAGATTA	1386
TCAGTGAGCA TTTCAGTATG TGTTTTAAGC CTAATCATTAA AAAGGAAATG GCTCATCTTA	1446
GACGTAGCAA CCGATGTAA TTTTCCCCCA GGCATCTCTC AGAGGGACTT GAATGTTAAA	1506
ATCATGTAA ATTTCTCCT TGGCTATGTT ATTTCTCATG GCTATGTTAT TCCTATTCGT	1566
ATTTCAATTA AAGGGACGGA ATATTTATTG TATTTCTGAA CTTTTTCAGG CATGCATCCG	1626
GGTCTTTGAA TAAAACACTA AGACTCCTTC TAGTAATGTT TGTAATCCTG TCTGTATCGA	1686
ATGTCTTTGA AAACGCAGTG ACTAAGCCAT AAATAATCTT CCACAGAACG TCCAGTGGTT	1746
CATGAACTTT GTATGTGGGG GTGGGGCAAG AATTGTCTCA CTATTGGTCA AGGAAGAGAA	1806
GGTAAGGTAT GCAAGGGTGG TTTAATCTTC TTCCGTGGAA GGACAAAATC ATCTATCATT	1866
TCCTCTGATC TCTATGCATT TGTTTGTTTT GAACTGAATC TGAATGAGC AAGAGTTGGC	1926
GTCCTGTGTT CTGAGGAAAC TCTTTGTCCT GCAGTCAGTG ACTAAAAGTG CTGAGAGATC	1986
TGAAGAGCAC TCTGAATCTG CCATATTTTT AATAGATGCT TTGTCTTCTC TTTGAATTC	2046
TTCCAG CCT AGT CAT TGT TGG TTA CGA GAT ATG GTA ACA CAC TTA TCA	2094
Pro Ser His Cys Trp Leu Arg Asp Met Val Thr His Leu Ser	
40 45 50	
GTC AGC TTG ACT ACT CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC	2142
Val Ser Leu Thr Thr Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly	
55 60 65	
TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GGG AAA ATA GTG GAT GAC	2190
Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Gly Lys Ile Val Asp Asp	
70 75 80 85	
CTC GTG GCA TGT ATG GAA GAA AAT GCA CCT AAG GTAACCTGGT ATTCATCAGA	2243
Leu Val Ala Cys Met Glu Glu Asn Ala Pro Lys	
90 95	
ATTATTTTTT TTATACTGAG CTCATGATGA GCAATTCACA ACCACTTGTA ATTCCAGCTC	2303
CAGAGGACAT TATCCCCTCT TTGGATGCCA TAGGAATCTG CTCTCAAATA TGTAAGATACC	2363
ACCTCTGCCA CCTCAGCACA TACATACACA TAATTAAAAA ATAGAAACAT TAAAGGAGTT	2423
CCAATCAATC CTTATTCTTT TCTGTATTCA GTATGCCAG ATGTAAATTC TAGGAATATG	2483
TTTTAAAGGC TAATTCTTAT TTTGTAATAA GCAGCTTTAA AATTCTTAAT TGTTTTTTTCG	2543
GGTCACTTTA TTGTCTTATT GCCACGACAT TGTCTGTCC CATTGTCTGT TATTCCTTCT	2603
GTTTTGTTTA TTGTCCCTA GTTACTTTGA TCATGAGATT GACCTGTTAC CCGTTGTTAT	2663
TCTCTGTAGC CATTTTGAGT TGTGTCTATT AGAACAGCTG TTAAATTACT TGAATCATTG	2723

AGGACATAGT CAATAATCTA TTATGCTGAT CCAGTCAAGT CTATGAGTTA TTTGAAAACT	2783
AGAATCTTTG TTAATTATTT GTTTGCTTGT TTGTTTGTTC ATTATTTGTC TAG AAT Asn	2839
GTA AAA GAA TCA CTG AAG AAG CCA GAA ACT AGA AAC TTT ACT CCT GAA Val Lys Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu 100 105 110	2887
GAA TTC TTT AGT ATT TTC AAT AGA TCC ATT GAT GCC TTC AAG GAC TTC Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe 115 120 125	2935
ATG GTG GCA TCT GAC ACT AGT GAT TGT GTG CTC TCT TCA ACA TTA GGT Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Ser Thr Leu Gly 130 135 140 145	2983
CCT GAG AAA G GTAAGGCTTT TAAGCATTTT TTGTTTAAAT GTACATAGAA Pro Glu Lys	3033
AGCCTGAACT TCTGTAAGCC TCTACTGCTG AATCAACTAA ATGTGTTGCT GTAGAAAGAA	3093
CGTGTGGGTT TTTCTGATAA AAACAAAAAG CAAATATCAA TGACTACCAA TGATTATTAT	3153
CTAGCTTGAG AGATATGCCC TAAGACAGCG ATTCTCGATA TTTCTAAATT AAAGAATTGT	3213
GTGATGGTGG CTCACATATT TTCTAACTGT GATATTTGCC AGGAGAGTAG AATAATGTTA	3273
TTCTTCATCC CCAGAATTCC TAAGATTTCA CGTCTCATGT CTTTTCATA AGGTTCAAAC	3333
TCTGAGACTT GAGTTCTGAG CCTCAGCAGG TCATTCTGAA TCCCCACTCT CCCCAGCTG	3393
GGTCCCTATG GGGGAACTAA CTTCATTGCT TTCTTTTAAA ACATGACGAG TTACCAACAG	3453
CTCCTCGCTA TTATAAACAT GTTCCTAAGC ATGTCTGTGC ATGCAATAAG CCTTCACTCT	3513
ACAAGACAGT TATGGTGTAT CGCTTGACAA AACTGAGCAG CCAAGCTGAG TATGAAATAA	3573
TAATCTAGAC TTGGGAGGCA GACCCAGCAC CTACTGTGAT ATTGCACTTC GCCTTTGGGG	3633
GACTCTATGA TTCAAAGTT CACCATGTAA CACTGACACA TTATTGCTTT CTATTTAG AT Asp	3693
TCC AGA GTC AGT GTC AGA AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC Ser Arg Val Ser Val Arg Lys Pro Phe Met Leu Pro Pro Val Ala Ala 150 155 160 165	3741
AGT TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT AGTAAGTACA CATATCTGAT Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn 170 175	3794
TTACTGCATG CATGGCTCCA AGTATCCTCT ATAGGAGTGT TGCATGGACT TAAAGTTTAT	3854

AAATCACTAC TAATAATGCT GTTCTGTCAC TGTATTCCT TGTATGGGCT TCCTGACAAT	3914
TAAATATCTG GTTTGTAGAA TCGGATCTCC TTAGAGGTTA AGATGACCAT GACAAAATTA	3974
GGCCAATCAA CTTTCTGCGA AGGTTATTTT AAATAAGGCA CGAAATTAAT TGAAGGAAAA	4034
AAAAATACAA GCAAGGCCTT ATTTTGAATC ATGGTAGGCT TAAAATAGAC TTTGTGGAGA	4094
ATGTCCCTGA TCAAAGTGGA GTTTTCAGAT TTCAAGTGCA TGTGCTAACT CTCCACAATG	4154
TCAAGGCTAT TTTCAGTTTT GTGTCTCCAT ATTTACTACT GCATGTTTGG AAATTTGCTG	4214
ATGCTGTTAG ATTACCTAAG AATGTATGTT GAAGAAGAAT GGACTTCTTT CCCTAAAATT	4274
TCTGTCCTCT TTGCCCAAGA ACCCACGTTC CTGGAAGACT ATCTTATTTT CATGTCTGTG	4334
CAATGATCAT TATAAAGATT ATTGAATATA CTGGGAATAC TCTGGTTTCT GTTTTTACAG	4394
ATTCATAATA GCTTATTCAG TCTTTAAAGA AAGTTCTCTG AAGTCCATGC TTTAGAATGT	4454
TTCTCTATCA AAACCTGACC TGGACCTTAA ATAAAGCTAT ATTTAGTCTT TTTATCCCTG	4514
AAAAATATAT TTCACAGTGT AGACATTTGA TATACATCTA AGGGAAGGAT GCTGCCAGAA	4574
TGCTCGGGCT GGCAGTCTAC AAAGTCCACT GCTCTCAGGA TGGACTTCTG AAAGCGGAAA	4634
TTGTGAACTG CATGCATATA ACATATCAGA TCCTCGAGC	4673

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro	
-20	-15 -10 -5
Leu Val Lys Thr Gln Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val	
	1 5 10
Lys Asp Ile Thr Lys Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile	
	15 20 25
Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu Pro Ser His Cys Trp	
	30 35 40
Leu Arg Asp Met Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Leu	
	45 50 55 60



Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile  
65 70 75

Asp Lys Leu Gly Lys Ile Val Asp Asp Leu Val Ala Cys Met Glu Glu  
80 85 90

Asn Ala Pro Lys Asn Val Lys Glu Ser Leu Lys Lys Pro Glu Thr Arg  
95 100 105

Asn Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp  
110 115 120

Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu  
125 130 135 140

Ser Ser Thr Leu Gly Pro Glu Lys Asp Ser Arg Val Ser Val Arg Lys  
145 150 155

Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser  
160 165 170

Ser Ser Ser Asn  
175

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 26..844

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 101..844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTGGATCGCA GCGCTGCCTT TCCTT ATG AAG AAG ACA CAA ACT TGG ATT ATC	52
Met Lys Lys Thr Gln Thr Trp Ile Ile	
-25 -20	
ACT TGC ATT TAT CTT CAA CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT	100
Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro Leu Val Lys Thr	
-15 -10 -5	
CAG GAG ATC TGC AGG AAT CCT GTG ACT GAT AAT GTA AAA GAC ATT ACA	148
Gln Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val Lys Asp Ile Thr	
1 5 10 15	

AAA CTG GTG GCG AAT CTT CCA AAT GAC TAT ATG ATA ACC CTC AAC TAT Lys Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile Thr Leu Asn Tyr 20 25 30	196
GTC GCC GGG ATG GAT GTT TTG CCT AGT CAT TGT TGG TTA CGA GAT ATG Val Ala Gly Met Asp Val Leu Pro Ser His Cys Trp Leu Arg Asp Met 35 40 45	244
GTA ACA CAC TTA TCA GTC AGC TTG ACT ACT CTT CTG GAC AAG TTT TCA Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Leu Asp Lys Phe Ser 50 55 60	292
AAT ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GGG Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Gly 65 70 75 80	340
AAA ATA GTG GAT GAC CTC GTG GCA TGT ATG GAA GAA AAT GCA CCT AAG Lys Ile Val Asp Asp Leu Val Ala Cys Met Glu Glu Asn Ala Pro Lys 85 90 95	388
AAT GTA AAA GAA TCA CTG AAG AAG CCA GAA ACT AGA AAC TTT ACT CCT Asn Val Lys Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro 100 105 110	436
GAA GAA TTC TTT AGT ATT TTC AAT AGA TCC ATT GAT GCC TTC AAG GAC Glu Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp 115 120 125	484
TTC ATG GTG GCA TCT GAC ACT AGT GAT TGT GTG CTC TCT TCA ACA TTA Phe Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Ser Thr Leu 130 135 140	532
GGT CCT GAG AAA GAT TCC AGA GTC AGT GTC ACA AAA CCA TTT ATG TTA Gly Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu 145 150 155 160	580
CCC CCT GTT GCA GCC AGT TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn 165 170 175	628
AGG AAA GCC GCA AAG TCC CCT GAA GAC CCA GGC CTA CAA TGG ACA GCA Arg Lys Ala Ala Lys Ser Pro Glu Asp Pro Gly Leu Gln Trp Thr Ala 180 185 190	676
ATG GCA CTG CCG GCT CTC ATT TCG CTT GTA ATT GGC TTT GCT TTT GGA Met Ala Leu Pro Ala Leu Ile Ser Leu Val Ile Gly Phe Ala Phe Gly 195 200 205	724
GCC TTA TAC TGG AAG AAG AAA CAG TCA AGT CTT ACA AGG GCA GTT GAA Ala Leu Tyr Trp Lys Lys Lys Gln Ser Ser Leu Thr Arg Ala Val Glu 210 215 220	772
AAT ATA CAG ATT AAT GAA GAG GAT AAT GAG ATA AGT ATG TTG CAA CAG Asn Ile Gln Ile Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Gln 225 230 235 240	820

AAA GAG AGA GAG TTT CAA GAG GTG TAATT  
Lys Glu Arg Glu Phe Gln Glu Val  
245

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Ile	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	-25	-20	-15	-10
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Gln	Glu	Ile	Cys	Arg	Asn	Pro	-5	1	5	
Val	Thr	Asp	Asn	Val	Lys	Asp	Ile	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	10	15	20	
Asn	Asp	Tyr	Met	Ile	Thr	Leu	Asn	Tyr	Val	Ala	Gly	Met	Asp	Val	Leu	25	30	35	
Pro	Ser	His	Cys	Trp	Leu	Arg	Asp	Met	Val	Thr	His	Leu	Ser	Val	Ser	40	45	50	55
Leu	Thr	Thr	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	60	65	70	
Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Gly	Lys	Ile	Val	Asp	Asp	Leu	Val	75	80	85	
Ala	Cys	Met	Glu	Glu	Asn	Ala	Pro	Lys	Asn	Val	Lys	Glu	Ser	Leu	Lys	90	95	100	
Lys	Pro	Glu	Thr	Arg	Asn	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Ser	Ile	Phe	105	110	115	
Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Phe	Met	Val	Ala	Ser	Asp	Thr	120	125	130	135
Ser	Asp	Cys	Val	Leu	Ser	Ser	Thr	Leu	Gly	Pro	Glu	Lys	Asp	Ser	Arg	140	145	150	
Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	155	160	165	
Leu	Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Ala	Lys	Ser	Pro	170	175	180	

Glu Asp Pro Gly Leu Gln Trp Thr Ala Met Ala Leu Pro Ala Leu Ile  
 185 190 195

Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Lys  
 200 205 210 215

Gln Ser Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu  
 220 225 230

Asp Asn Glu Ile Ser Met Leu Gln Gln Lys Glu Arg Glu Phe Gln Glu  
 235 240 245

Val

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(905..1018, 1914..1976, 2572..2742, 3152  
 ..3307, 3513..3595)

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: join(965..1018, 1914..1976, 2572..2742, 3152  
 ..3307, 3513..3595)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CACAAGTGAG TAGGGCGCGC CCGGGAGCTC CCAGGCTCTC CAGGAAAAAT CGCGCCCGGT 60

GCCCCGGGGA AGCCGGCGCT CCCTGGGACT TGCAGCTGGG GCGTGCAGGG CTGTGCCTGC 120

CGGGTGAGAT ACTACAAAGA TAAATCAGTT GCACAAGTTC TTGAAACTCT ACAGTGTAAT 180

AAGGAAAAAT AAGTCATGCA TAAAAGCAAC TATAATACAT AATAGAAAAT GTTATTTTCA 240

AGCCGATGTG TAGGTTATGT GTGTTCGAGA GAGAGAGAGA GAAGACAGAT TACTTTCTGC 300

TAGGGTTCAA GAATGCCTTC CTGTTGGCTA AGGAAATATT TTCCTTAAGT GGCTAAAAAG 360

CTGTGTTTCA AAATATTCTT TTGATGTCTC ACAAATTCAG TGGAATTCTC TTAGGTCTAA 420

AAATATACAT CTCTCTCACT TTAACCTGGT GTGCTATTGT AGATTATTGG ATTAAAGCAC 480

TGCTCAGGGA TTATGCTGCT TCTTGCCAAG CAGTCTACAT TTAAAGTAGA AATAAGATGT 540

TTCTTTTGGT GCCATAAGGT ATACATTTTA TGCATTCTCT AGTTTTTTAGA AGATACCCTA 600

AGGGCTAAGT CTTTAACATG CTGCTACAAG TTTATTCCTA ATTGCCATTG GGAAATTGGC	660
TGAAGAAAGT TTTTAACAAA AGTTAACAAT ATTGTCATTG AGAGAATAAT TCAAAATGGA	720
TTTTAACTAA AAGCTTTTAA AAACCTTTGGT GAGCATAGCT TGAATGCGTA ATATTTAATT	780
GCATTTAAGC CAATAACATA TATTAGACTG GTCTTTTTGT GCATCAAGGC ATTAGATGTT	840
AAAAGTTTGA ATGATTACAG ATCTTAACTG ATGATCACCA AGCAATTTTT CTGTTTTCAT	900
TTAG ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG CTG CTC CTA TTT AAT	949
Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu Leu Phe Asn	
-20 -15 -10	
CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG AAT CGT GTG ACT AAT AAT	997
Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg Val Thr Asn Asn	
-5 1 5 10	
GTA AAA GAC GTC ACT AAA TTG GTAAGTAAGG AATGCTTTAC CGTGCTGTGT	1048
Val Lys Asp Val Thr Lys Leu	
15	
AAAAAAGAGC TGTGGCTCTT TTTCTGTGTC TTGTTGATAA AAGATTTAGA TTTTTCTTGC	1108
CCCAAAGTAA TGTTTTCTTA AAGTGGGGAA AGTAATCACT GGGTTACAAT AAAGGGTTTA	1168
TAGAAAGCAG GTAGTGAGAT ATTTAGGGTC ATGGATAATT TGTTGGTAAA ACTGGCTAGT	1228
TGCACACCAC TGCTGTGACT GCTTCTTTGC TGGTCTTCTC CCCATCCTTC ATAGGCAGTG	1288
AAGGACCTTG GAGAGTTCGC TGTGTGCTGA TGGGCTTGCC CCAGCTTGTT CCCATAATC	1348
TCTCCAGTGG GTTTCCCAGC ATGTTCTATT CCCCTTCACA TGTCTTCCTA CTCTTCTTTA	1408
AAAAGCCTAA CGAAAGGAAA TCTGAAATGG CTATTCTCCC AATTCAATCA GCAGGAAGAC	1468
CCTGTCACAT GTCAGTGGGT GTTTGCTCCT TCAGGGAACA TAGAGAGGTG ATTCATTGCC	1528
CACATGTTGA AGGGACTCAT CTCCCTGGTT TGTCACATTG AACTCTTCCC TCAGCGAAAG	1588
CATTTGCATT GCTTCCCGAA TTCCAAGATC ACAGGTGGAA GCTGAAATTC AGATCATGTT	1648
TCCAAACTC AGTAGGTTAT ACCTAGCCAG GCATAACTGA ATTTGGAGTC TAAAAGATCT	1708
GTATTATCAC TTTTTTATTT TGAAGGATGC CTTTGTATTA CAGAGGGAAA TCAAGGATTA	1768
AAAATCAATA TACATGTAAA TATTGAAATT CATTGGTAAC TTTAAAAAGC ACAACAGTTT	1828
TGTGTGCTTT TCTCCAAAGC ACTACAAATA TGATTAATTG ATGTATAAGA ATTTTCTTAT	1888
GGAATTTTTT TTTTGTCTC TGTAG GTG GCA AAT CTT CCA AAA GAC TAC ATG	1940
Val Ala Asn Leu Pro Lys Asp Tyr Met	
20 25	

ATA ACC CTC AAA TAT GTC CCC GGG ATG GAT GTT TTG GTATGTAAAC	1986
Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu	
30 35	
TACATTTCTG AGTTTCATTT TAGTAGCTCA TAGAAGAAAT GGGATCATTG ATATTGAGAT	2046
AGTACACTAG CTGCTATTTA GGAGCTTGCT TATTGTCAGG ATTTGAAGAA TTTATCTTTG	2106
GAATTTGACT TGCAGGCTTT TTTTCCCCC TCTTCCTGTT ACAAGAGTCC CTCCTCCTAT	2166
TACAATAGTC CCTCCTCCTC CTGTCACACT AGTCCCTTCT CTTCTGTGTA CAATAACCCC	2226
TGTCCTCCTA TTACAACATT TTAAGTAATG TAATATTAAT TTTAAAAATC TGGCCAGGCA	2286
CGGTGGTTCA TGCTTGTAAT CCCAGCACAT TGGGAAGCTG AGACGGGTGG ATCATTGAG	2346
GTCAGGAAGT TTGAGACAGC CTGGCCAACA TGGTGAAACT TCCTCTCTAC TAAAAATAAA	2406
AAAGTAGCCA GGCATGGTGG CAGGCACTTG TAATCTGAGC TACTCGAGAG GCTGAGGCAG	2466
GAGAATCACT TGAGTAACTA AAACGATAGC TTTGAAGAGT ACTCCGAGTT TTATGGCACT	2526
TACTTATTAA AATAGCTGTT TTGTCTCTTT TTTTCATATCT TGCAG CCA AGT CAT	2580
Pro Ser His	
40	
TGT TGG ATA AGC GAG ATG GTA GTA CAA TTG TCA GAC AGC TTG ACT GAT	2628
Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser Leu Thr Asp	
45 50 55	
CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC TTG AGT AAT TAT TCC	2676
Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser	
60 65 70	
ATC ATA GAC AAA CTT GTG AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG	2724
Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val Glu Cys Val	
75 80 85 90	
AAA GAA AAC TCA TCT AAG GTAACCTTGT GTTCATTGGG ATTATTTTTTC	2772
Lys Glu Asn Ser Ser Lys	
95	
ATTACGCTTC TCTAAAAACC CATGCTTCTT GGTGCTGTTG GGGAAATGA GGCACCTTTA	2832
TTTATGATAT TTTGATTGTA TAAACTTCAA ATTTAAAAAT CTTGTTTCTG TGAGCAAAGA	2892
AAACAAGTAT TTGCAGTTAT ACTGCAATAC TGAAGTGCAC ATTCTTGTGT TCACTGCCCC	2952
AGATTCAACT TGTGATCCCA CTGGGATCAC TACCCTGCAT TACCAATCTG AATTACATAC	3012
GTTAAAACAG CCATCTAAAA GTGCTAGTTG TAAGAGTCTA AATACTTGAA TCTTTGAGAG	3072
ACATATTTAT AGTCCATTAT CTTACCTCA GTTAAGTCTG AAGACTATTT GAAAAATGTA	3132

ATCCTATTTT TTCTTCTAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro 100 105	3184
AGG CTC TTT ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile 110 115 120	3232
GAT GCC TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val 125 130 135	3280
GTT TCT TCA ACA TTA AGT CCT GAG AAA GGTAAGACAT GTAAGCATTT Val Ser Ser Thr Leu Ser Pro Glu Lys 140 145	3327
CCAGTTCAAA TGTAACAAC AAACCTAAAT CTTCCCTATG TAGTAAGAAT CTACCTCTGT	3387
GTTAAGCTGT AGCAAGATAC ATGCATGTAC GTCTAATAAA AAAGCAGATA TCAATAGCAC	3447
AGAAGAAACT CTATAACTCA TACAAATCAC CATATAACAC TGACACATTA TTGCTTTCTA	3507
TTTAG ATT CCA GAG TCA GTG TCA CAA AAC CAT TTA TGT TAC CCC CTG Ile Pro Glu Ser Val Ser Gln Asn His Leu Cys Tyr Pro Leu 150 155 160	3554
TTG CAG CCA GCT CCC TTA GGA ATG ACA GCA GTA GCA GTA ATAGTAAGTA Leu Gln Pro Ala Pro Leu Gly Met Thr Ala Val Ala Val 165 170 175	3603
CATATATCTG ATTTAATGCA TGCATGGCTC CAATTAGCAC CTATAGGAGT ATTGCATGGG	3663
CTTTCAAGGA AACTTCTACA TTTATTATTA TTGATACTGT TCTGTTACTG TTATTCCTTT	3723
TATGGTCTTC TTGAGACTTA AGTTTGTAGA ATTAAATTC CCTAGAGCTG GAGATAATGT	3783
TTAGAGAATT AGGCCAATAA ATTT	3807

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 195 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro -20 -15 -10 -5
Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg Val Thr Asn Asn Val 1 5 10

Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro Lys Asp Tyr Met Ile  
 15 20 25  
 Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu Pro Ser His Cys Trp  
 30 35 40  
 Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu  
 45 50 55 60  
 Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile  
 65 70 75  
 Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu  
 80 85 90  
 Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg  
 95 100 105  
 Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp  
 110 115 120  
 Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val  
 125 130 135 140  
 Ser Ser Thr Leu Ser Pro Glu Lys Ile Pro Glu Ser Val Ser Gln Asn  
 145 150 155  
 His Leu Cys Tyr Pro Leu Leu Gln Pro Ala Pro Leu Gly Met Thr Ala  
 160 165 170  
 Val Ala Val  
 175

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 17..640

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 92..640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:



AAGCTTGCCT TTCCTT ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC	49
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys	
-25 -20 -15	
ATT TAT CTT CAG CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG	97
Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly	
-10 -5 1	
ATC TGC AGG AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG	145
Ile Cys Arg Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu	
5 10 15	
GTG GCA AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC	193
Val Ala Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro	
20 25 30	
GGG ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA	241
Gly Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val	
35 40 45 50	
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT ATT	289
Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile	
55 60 65	
TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG AAT ATA	337
Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile	
70 75 80	
GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT AAG GAT CTA	385
Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu	
85 90 95	
AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT ACT CCT GAA GAA	433
Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu	
100 105 110	
TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC TTC AAG GAC TTT GTA	481
Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val	
115 120 125 130	
GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT TCT TCA ACA TTA AGT CCT	529
Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro	
135 140 145	
GAG AAA GAT TCC AGA GTC AGT GTC ACA AAA CCA TTT ATG TTA CCC CCT	577
Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro	
150 155 160	
GTT GCA GCC AGC TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT AGT AAG	625
Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser Lys	
165 170 175	
TAC ATA TAT CTG ATT TAATGCATGC ATGGCTCCAA TTAGCACCTA TAGGAGTATT	680
Tyr Ile Tyr Leu Ile	
180	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Leu	Thr	Cys	Ile	Tyr	Leu	Gln	Leu
-25					-20					-15					-10
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Glu	Gly	Ile	Cys	Arg	Asn	Arg
				-5					1				5		
Val	Thr	Asn	Asn	Val	Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro
		10					15					20			
Lys	Asp	Tyr	Met	Ile	Thr	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu
	25					30					35				
Pro	Ser	His	Cys	Trp	Ile	Ser	Glu	Met	Val	Val	Gln	Leu	Ser	Asp	Ser
40					45					50					55
Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser
				60					65					70	
Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	Asn	Ile	Val	Asp	Asp	Leu	Val
			75					80					85		
Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser	Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys
		90					95					100			
Ser	Pro	Glu	Pro	Arg	Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe
	105					110					115				
Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr
120					125					130					135
Ser	Asp	Cys	Val	Val	Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg
				140					145					150	
Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser
			155					160					165		
Leu	Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Ser	Lys	Tyr	Ile	Tyr	Leu	Ile
		170					175					180			

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(565..579, 1684..1797, 2693..2755, 3351..3521, 3932..4088, 4314..4397, 4778..4887, 5208..5275, 5677..5713)

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: join(1744..1797, 2693..2755, 3351..3521, 3932..4088, 4314..4397, 4778..4887, 5208..5275, 5677..5713)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```
GAGCTCCGAG CCCTCTCTGG CGCGCGAGGT ATTTCTGTCTG TNCCCGGGGG TGCCAGGTGA      60
GCCCCAGCGG ATCCGGGAGG GTAAGCTGGG ACTCCTCGCG AGCAGTAGCT GCAGGGTACC      120
AAGCTTCGCC CTCTGCGTCC CCGCGCCTTC GCGGTCTCCC GCCAGTGCAG GTCCGGGGCC      180
CCCAGGCGAG CGGACAAGGT TGGCCTAATC TGCCAAACTT CTGGGGCATT TACCGTGCTC      240
TGGCCGCCCT CCCGATTCTT CCCTCCGCGC CCTTGCCCTG TTCTCGCCTA CCCCAGGCTC      300
CGGAAGGGAA GGAGGCGTGT CCGGAGCAGG CGGGCGGGAA CTGTATAAAA GCGCCGGCGG      360
CTCAGCAGCC GGCTTCGCTC GCCGCCCTGC GCCGAGACTA GAAGCGCTGC GGGGAAGCAGG      420
GACAGTGGAG AGGGCGCTGC GCTCGGGCTA CCAATGCGT GGAATATCTG CCGCCGCTGT      480
TCGTGCAATA TGCTGGAGCT CCAGAACAGC TAAACGGAGT CGCCACACCA CTGTTTGTGC      540
TGGATCGCAC CGCTGCCTTT CCTT ATG AAG AAG ACA CAA GTGAGTAGGG      589
                               Met Lys Lys Thr Gln
                               -25

CGGCCCCGGG AGCTCCCAGG CTCTCCAGGA AAAATCGCGC CCGGTGCCCC GGGGAAGCCG      649
GCGCTCCCTG GGAATTGCAG CTGGGGCGTG CAGGGCTGTG CCTGCCGGGT GAGACAAGAG      709
GATGCGGGGG AGGCCGGCGT GGTGTGTGAT CCCGAGCCGA GCCGNNTGAG CCAGGGAGAA      769
AAGGAGTGGG AGTACTGAGA GGGAGCCAGT GTCAAGTTTG GAGCCTCAGC AGTTAAGTTT      829
TGAGCTGTCA GTCGAAACC GTAATTCCCG TCTGGTGGA AGATTGGCTT TTNGNCCACG      889
```

GAATGTAAGT TATCACAGAT ACTACAAAGA TAAATCAGTT GCACAAGTTC TTGAAACTCT	949
ACAGTGTAAT AAGGAAAAAT AAGTCATGCA TAAAAGCAAC TATAATACAT AATAGAAAAT	1009
GTTATTTTCA AGCCGATGTG TAGGTTATGT GTGTTGAGA GAGAGAGAGA GAAGACAGAT	1069
TACTTCTGCT TAGGGTTCAA GAATGCCTTC CTGTTGGCTA AGGAAATATT TTCCTTAAGT	1129
GGCTAAAAAG CTGTGTTTCA AAATATTCTT TTGATGTCTC ACAAATTCAG TGGAATTCTC	1189
TTAGGTCTAA AAATATACAT CTCTCTCACT TTAAGTTGGT GTGCTATTGT AGATTATTGG	1249
ATTAAAGCAC TGCTCAGGGA TTATGCTGCT TCTTGCCAAG CAGTCTACAT TTAAAGTAGA	1309
ATAAAGATGT TTCTTTTGGT GCCATAAGGT ATACATTTTA TGCATTCTCT AGTTTTTAGA	1369
AGATACCCTA AGGGCTAAGT CTTTAACATG CTGCTACAAG TTTATTCCTA ATTGCCATTG	1429
GGAAATTGGC TGAAGAAAGT TTTTAACAAA AGTTAACAAT ATTGTCATTG AGAGAATAAT	1489
TCAAATGGA TTTTAACATA AAGCTTTTAA AAAGTTTGGT GAGCATAGCT TGAATGCGTA	1549
ATATTTAATT GCATTTAAGC CAATAACATA TATTAGACTG GTCTTTTTGT GCATCAAGGC	1609
ATTAGATGTT AAAAGTTTGA ATGATTACAG ATCTTAACTG ATGATCACCA AGCAATTTTT	1669
CTGTTTTTCAT TTAG ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG CTG CTC	1719
Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu Leu	
-20 -15 -10	
CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG AAT CGT GTG	1767
Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg Val	
-5 1 5	
ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTAAGTAAGG AATGCTTTAC	1817
Thr Asn Asn Val Lys Asp Val Thr Lys Leu	
10 15	
CGTGCTGTGT AAAAAAGAGC TGTGGCTCTT TTTCCTGTGC TTGTTGATAA AAGATTTAGA	1877
TTTTTCTTGC CCCAAAGTAA TGTTTTCTTA AAGTGGGGAA AGTAATCACT GGGTTACAAT	1937
AAAGGGTTTA TAGAAAGCAG GTAGTGAGAT ATTTAGGGTC ATGGATAATT TGTTGGTAAA	1997
ACTGGCTAGT TGCACACCAC TGCTGTGACT GCTTCTTTGC TGGTCTTCTC CCCATCCTTC	2057
ATAGGCAGTG AAGGACCTTG GAGAGTTGCG TGTGTGCTGA TGGGCTTGCC CCAGCTTGTT	2117
CCCCATAATC TCTCCAGTGG GTTTCCCAGC ATGTTCTATT CCCCTTCACA TGTCTTCCTA	2177
CTCTTCTTTA AAAAGCCTAA CGAAAGGAAA TCTGAAATGG CTATTCTCCC AATTCAATCA	2237
GCAGGAAGAC CCTGTCACAT GTCAGTGGGT GTTTGCTCCT TCAGGGAACA TAGAGAGGTG	2297
ATTCATTGCC CACATGTTGA AGGGACTCAT CTCCCTGGTT TGTCACATTG AACTCTTCCC	2357

TCAGCGAAAG CATTTCGATT GCTTCCCGAA TTCCAAGATC ACAGGTGGAA GCTGAAATTC	2417
AGATCATGTT TCCAAAACCTC AGTAGGTTAT ACCTAGCCAG GCATAACTGA ATTTGGAGTC	2477
TAAAAGATCT GTATTATCAC TTTTATTATT TGAAGGATGC CTTTGTGATTA CAGAGGGAAA	2537
TCAAGGATTA AAAATCAATA TACATGTAAA TATTGAAATT CATTGGTAAC TTTAAAAAGC	2597
ACAACAGTTT TGTGTGCTTT TCTCCAAAGC ACTACAAATA TGATTAATTG ATGTATAAGA	2657
ATTTTCTTAT GGAATTTTTT TTTTGTCTC TG TAG GTG GCA AAT CTT CCA AAA	2710
Val Ala Asn Leu Pro Lys	
20	
GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG ATG GAT GTT TTG	2755
Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu	
25 30 35	
GTATGTAAAC TACATTTCTG AGTTTCATTT TAGTAGCTCA TAGAAGAAAT GGGATCATTC	2815
ATATTGAGAT AGTACACTAG CTGCTATTTA GGAGCTTGCT TATTGTCAGG ATTTGAAGAA	2875
TTTATCTTTG GAATTTGACT TGCAGGCTTT TTTTCCCCC TCTTCCTGTT ACAAGAGTCC	2935
CTCCTCCTAT TACAATAGTC CCTCCTCCTC CTGTCACACT AGTCCCTTCT CTTCTGTTA	2995
CAATAACCCC TGTCCTCCTA TTACAACATT TTAAGTAATG TAATATTAAT TTTAAAAATC	3055
TGGCCAGGCA CGGTGGTTCA TGCTTGTAAT CCCAGCACAT TGGGAAGCTG AGACGGGTGG	3115
ATCATTTGAG GTCAGGAAGT TTGAGACAGC CTGGCCAACA TGGTGAAACT TCCTCTCTAC	3175
TAAAAATAAA AAAGTAGCCA GGCATGGTGG CAGGCACTTG TAATCTGAGC TACTCGAGAG	3235
GCTGAGGCAG GAGAATCACT TGAGTAATA AAACGATAGC TTTGAAGAGT ACTCCGAGTT	3295
TTATGGCACT TACTTATTAA AATAGCTGTT TTGTCTCTTT TTTCATATCT TGCAG CCA	3353
Pro	
40	
AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA CAA TTG TCA GAC AGC TTG	3401
Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser Leu	
45 50 55	
ACT GAT CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC TTG AGT AAT	3449
Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn	
60 65 70	
TAT TCC ATC ATA GAC AAA CTT GTG AAT ATA GTG GAT GAC CTT GTG GAG	3497
Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val Glu	
75 80 85	
TGC GTG AAA GAA AAC TCA TCT AAG GTAACCTTGT GTTCATTGGG ATTATTTTTC	3551
Cys Val Lys Glu Asn Ser Ser Lys	
90 95	

ATTACGCTTC TCTAAAAACC CATGCTTCTT GGTGCTGTTG GGGAAAATGA GGCACCTTTA	3611
TTTATGATAT TTTGATTGTA TAAACTTCAA ATTTAAAAAT CTTGTTCAGA TGAGCAAAGA	3571
AAACAAGTAT TTGCAGTTAT ACTGCAATAC TGAAGTGCAC TATTCTTGTG TTCACTGCCC	3731
CAGATTCAAC TTGTGATCCC ACTGGGATCA CTACCCTGCA TTACCAATCT GAATTACATA	3791
CGTTAAAAACA GCCATCTAAA AGTGCTAGTT GTAAGAGTCT AAATACTTGA ATCTTTGAGA	3851
GACATATTTA TAGTCCATTA TCTTCACCTC AGTTAAGTCT GAAGACTATT TGAAAAATGT	3911
AATCCTATTT TTTCTTCTAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA	3961
Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu	
100 105	
CCC AGG CTC TTT ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC	4009
Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser	
110 115 120	
ATT GAT GCC TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT	4057
Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys	
125 130 135	
GTG GTT TCT TCA ACA TTA AGT CCT GAG AAA G GTAAGACATG TAAGCATTTT	4108
Val Val Ser Ser Thr Leu Ser Pro Glu Lys	
140 145	
CAGTTCAAAT GTAAACAACA AACTTAAATC TTCCCTATGT AGTAAGAATC TACCTCTGTG	4168
TTAAGCTGTA GCAAGATACA TGCATGTACG TCTAAAAAAA AGCAGATATC AATAGCACAG	4228
AAGAAACTAA TGATTGTAGA TTTGTGGGCT CTATAACTCA TACAAATCAC CATATAACAC	4288
TGACACATTA TTGCTTTCTA TTTAG AT TCC AGA GTC AGT GTC ACA AAA CCA	4339
Asp Ser Arg Val Ser Val Thr Lys Pro	
150 155	
TTT ATG TTA CCC CCT GTT GCA GCC AGC TCC CTT AGG AAT GAC AGC AGT	4387
Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser	
160 165 170	
AGC AGT AAT A GTAAGTACAT ATATCTGATT TAATGCATGC ATGGCTCCAA	4437
Ser Ser Asn	
175	
TTAGCACCTA TAGGAGTATT GCATGGGCTT TCAAGGAAAC TTCTACATTT ATTATTATTG	4497
ATACTGTTCT GTTACTGTTA TTCCTTTTAT GGTCTTCTTG AGACTTAAGT TTGTAGAATT	4557
AAATTTCCCT AGAGCTGGAG ATAATGTTTA GAGAATTAGG CCAATAAATT TTCTGCTGAG	4617
GTTATTTTAA ATAAGACATA AAATTAATTT TAGAAATATG ATTTATGCCT TTTGTTGAAT	4677
CATTAACATA TATACAGAAA CAGTTAAAC AACCACAGCA TAAGAGAAAA ACTTCTAGAA	4737

TGGATATGCT GTATTCATCA GTGTGTTCTT TAAATTATAG	GG AAG GCC AAA AAT	4791
	Arg Lys Ala Lys Asn	
	180	
CCC CCT GGA GAC TCC AGC CTA CAC TGG CCA GCC ATG GCA TTG CCA GCA		4839
Pro Pro Gly Asp Ser Ser Leu His Trp Pro Ala Met Ala Leu Pro Ala		
185 190 195		
TTG TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG		4887
Leu Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys		
200 205 210		
GTAAGTGGTA CCATTCCTTT TTTTAAAAAT ATGCTATGTT TACATAAATT ATCATCTTTT		4947
TTTCCTCAAG AAATGATCCT TTAAGAAAAC AGTGAATCTA CCTTAGCTTA TACTAAACAA		5007
AATTTAAATT TTATAAAGTT TCCTGTTTCT CATTATGTCT GGAGACAATC CCTCTAGCTG		5067
ATAATTCACG CTTAAGAATT AGGAACTAAA ACTGTTATTG GAGTTATTGC CATAAAAGAT		5127
AAAAGTGGAG TCCACTTACC TCTTAAATAT TAGACCATTC ATTGATTATT TTACAGTATA		5187
TGTCTTTCTT CTTTTTCCAG AAG AGA CAG CCA AGT CTT ACA AGG GCA GTT		5237
Lys Arg Gln Pro Ser Leu Thr Arg Ala Val		
215 220		
GAA AAT ATA CAA ATT AAT GAA GAG GAT AAT GAG ATA AG GTATTTTGTT		5285
Glu Asn Ile Gln Ile Asn Glu Glu Asp Asn Glu Ile Ser		
225 230 235		
TTGCTAAATG TGTGCCCCAAT CAAGCATGAC ATTGCCATTT CACACACTGT GTACCTGCCC		5345
ATAATGTCTT TAAGAAGTCC TCACTCATG ACAGTAGCTC CTAACCAGTG AGTCCCAACT		5405
CTATCCATGT TTCTGATGTC TCACTCTCTC TTCGTATGTG TATATGCATA TACAGAGAAA		5465
GAAATGTTTT AACTACTTGG AAAGACTACC TTAAGACAAA TGAAGTCTTC CCTCTTCCCT		5525
ATAGTAATAA GAAGGTAGGC TCCCCCATTC AATTTTGCAA TCTTCTGCTA CTATATTTAC		5585
AGAAAAGCTG CCTTTTACAA TGCCGAGATC ATGGTGTACC TCAGAATCTC TGACCAAGAG		5645
CAAATAAGCA TTTTTTCTTA TTGTTTTTCA G T ATG TTG CAA GAG AAA GAG AGA		5698
Met Leu Gln Glu Lys Glu Arg		
240		
GAG TTT CAA GAA GTG TAATTGTGGC TTGTATCAAC ACTGTTACTT TCGTACATTG		5753
Glu Phe Gln Glu Val		
245		
GTAAGTTTTT TTCTTCTTTC CTTTTTTTTT CTTTTTTTTT TTATACTTTA AGTTCTAGGG		5813
TACATGTGCA CAATGTGCAG GTTTGTTACG TATGTTTACA TGTGCCATGT T		5864

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Leu	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	
-25					-20					-15					-10	
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Glu	Gly	Ile	Cys	Arg	Asn	Arg	
			-5						1				5			
Val	Thr	Asn	Asn	Val	Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	
		10					15					20				
Lys	Asp	Tyr	Met	Ile	Thr	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	
	25					30					35					
Pro	Ser	His	Cys	Trp	Ile	Ser	Glu	Met	Val	Val	Gln	Leu	Ser	Asp	Ser	
40					45					50					55	
Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	
			60						65					70		
Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	Asn	Ile	Val	Asp	Asp	Leu	Val	
		75							80				85			
Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser	Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	
		90					95					100				
Ser	Pro	Glu	Pro	Arg	Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	
	105					110					115					
Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	
120					125					130				135		
Ser	Asp	Cys	Val	Val	Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg	
			140						145					150		
Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	
		155						160					165			
Leu	Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Lys	Asn	Pro	Pro	
		170					175						180			
Gly	Asp	Ser	Ser	Leu	His	Trp	Pro	Ala	Met	Ala	Leu	Pro	Ala	Leu	Phe	
	185					190					195					
Ser	Leu	Ile	Ile	Gly	Phe	Ala	Phe	Gly	Ala	Leu	Tyr	Trp	Lys	Lys	Arg	
200					205					210					215	



Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu  
220 225 230

Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu  
235 240 245

Val

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Leu	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	1	5	10	15
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Glu	Gly	Ile	Cys	Arg	Asn	Arg	20	25	30	
Val	Thr	Asn	Asn	Val	Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	35	40	45	
Lys	Asp	Tyr	Met	Ile	Thr	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	50	55	60	
Pro	Ser	His	Cys	Trp	Ile	Ser	Glu	Met	Val	Val	Gln	Leu	Ser	Asp	Ser	65	70	75	80
Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	85	90	95	
Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	Asn	Ile	Val	Asp	Asp	Leu	Val	100	105	110	
Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser	Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	115	120	125	
Ser	Pro	Glu	Pro	Arg	Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	130	135	140	
Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	145	150	155	160
Ser	Asp	Cys	Val	Val	Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg	165	170	175	
Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	180	185	190	

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro  
 195 200 205

Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe  
 210 215 220

Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg  
 225 230 235 240

Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu  
 245 250 255

Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu  
 260 265 270

Val

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu  
 1 5 10 15

Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg  
 20 25 30

Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro  
 35 40 45

Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu  
 50 55 60

Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser  
 65 70 75 80

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser  
 85 90 95

Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val  
 100 105 110

Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys  
 115 120 125

Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe  
 130 135 140

Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Phe	Ala	Val	Ala	Ser	Glu	Thr	145	150	155	160
Ser	Asp	Cys	Val	Val	Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg	165	170	175	
Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	180	185	190	
Leu	Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Lys	Asn	Pro	Thr	195	200	205	
Gly	Asp	Ser	Ser	Leu	His	Trp	Ala	Ala	Met	Ala	Leu	Pro	Ala	Phe	Phe	210	215	220	
Ser	Leu	Ile	Ile	Gly	Phe	Ala	Phe	Gly	Ala	Leu	Tyr	Trp	Lys	Lys	Arg	225	230	235	240
Gln	Pro	Ser	Leu	Thr	Arg	Ala	Val	Glu	Asn	Ile	Gln	Ile	Asn	Glu	Glu	245	250	255	
Asp	Asn	Glu	Ile	Ser	Met	Leu	Gln	Glu	Lys	Glu	Arg	Glu	Phe	Gln	Glu	260	265	270	
Val																			

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Ile	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	1	5	10	15
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Lys	Gly	Ile	Cys	Gly	Lys	Arg	20	25	30	
Val	Thr	Asp	Asp	Val	Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	35	40	45	
Lys	Asp	Tyr	Lys	Ile	Ala	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	50	55	60	
Pro	Ser	His	Cys	Trp	Ile	Ser	Val	Met	Val	Glu	Gln	Leu	Ser	Val	Ser	65	70	75	80
Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	85	90	95	

Asn Tyr Ser Ile Ile Asp Lys Leu Val Lys Ile Val Asp Asp Leu Val		
100	105	110
Glu Cys Thr Glu Gly Tyr Ser Phe Glu Asn Val Lys Lys Ala Pro Lys		
115	120	125
Ser Pro Glu Leu Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe		
130	135	140
Asn Arg Ser Ile Asp Ala Phe Lys Asp Leu Glu Thr Val Ala Ser Lys		
145	150	155 160
Ser Ser Glu Cys Val Val Ser Ser Thr Leu Ser Pro Asp Lys Asp Ser		
165	170	175
Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser		
180	185	190
Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Ser Asn Ser		
195	200	205
Ile Gly Asp Ser Asn Leu Gln Trp Ala Ala Met Ala Leu Pro Ala Phe		
210	215	220
Phe Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys		
225	230	235 240
Lys Gln Pro Asn Leu Thr Arg Thr Val Glu Asn Ile Gln Ile Asn Glu		
245	250	255
Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln		
260	265	270
Glu Val		

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Lys Thr Gln Thr Trp Ile Val Thr Cys Ile Tyr Leu Gln Leu Leu		
1	5	10 15
Phe Asn Pro Leu Val Lys Thr Lys Gly Leu Cys Arg Asn Arg Val Thr		
20	25	30
Asp Asp Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro Lys Asp		
35	40	45

Tyr	Lys	Ile	Ala	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	Pro	Ser	
50						55					60					
His	Cys	Trp	Ile	Ser	Val	Met	Val	Glu	Gln	Leu	Ser	Val	Ser	Leu	Thr	
65					70					75					80	
Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	
				85					90					95		
Ser	Ile	Ile	Asp	Lys	Leu	Val	Lys	Ile	Val	Asp	Asp	Leu	Val	Glu	Cys	
			100					105					110			
Val	Glu	Gly	His	Ser	Ser	Glu	Asn	Val	Lys	Lys	Ser	Ser	Lys	Ser	Pro	
		115					120					125				
Glu	Pro	Arg	Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	Asn	Arg	
	130					135					140					
Ser	Ile	Asp	Ala	Phe	Lys	Asp	Leu	Glu	Met	Val	Ala	Ser	Lys	Thr	Ser	
145					150					155					160	
Glu	Cys	Val	Val	Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg	Val	
				165					170					175		
Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	Leu	
			180					185					190			
Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Thr	Asn	Pro	Ile	Glu	Asp	
	195						200					205				
Ser	Ser	Ile	Gln	Trp	Ala	Val	Met	Ala	Leu	Pro	Ala	Cys	Phe	Ser	Leu	
	210					215					220					
Val	Ile	Gly	Phe	Ala	Phe	Gly	Ala	Phe	Tyr	Trp	Lys	Lys	Lys	Gln	Pro	
225					230					235					240	
Asn	Leu	Thr	Arg	Thr	Val	Glu	Asn	Ile	Gln	Ile	Asn	Glu	Glu	Asp	Asn	
				245					250					255		
Glu	Ile	Ser	Met	Leu	Gln	Glu	Lys	Glu	Arg	Glu	Phe	Gln	Glu	Val		
			260					265					270			

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 273 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Ile	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	1	5	10	15
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Gln	Glu	Ile	Cys	Arg	Asn	Pro	20	25	30	
Val	Thr	Asp	Asn	Val	Lys	Asp	Ile	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	35	40	45	
Asn	Asp	Tyr	Met	Ile	Thr	Leu	Asn	Tyr	Val	Ala	Gly	Met	Asp	Val	Leu	50	55	60	
Pro	Ser	His	Cys	Trp	Leu	Arg	Asp	Met	Val	Thr	His	Leu	Ser	Val	Ser	65	70	75	80
Leu	Thr	Thr	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	85	90	95	
Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Gly	Lys	Ile	Val	Asp	Asp	Leu	Val	100	105	110	
Ala	Cys	Met	Glu	Glu	Asn	Ala	Pro	Leu	Asn	Val	Lys	Glu	Ser	Leu	Lys	115	120	125	
Lys	Pro	Glu	Thr	Arg	Asn	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Ser	Ile	Phe	130	135	140	
Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Phe	Met	Val	Ala	Ser	Asp	Thr	145	150	155	160
Ser	Asp	Cys	Val	Leu	Ser	Ser	Thr	Leu	Gly	Pro	Glu	Lys	Asp	Ser	Arg	165	170	175	
Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	180	185	190	
Leu	Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Ala	Lys	Ser	Pro	195	200	205	
Glu	Asp	Pro	Gly	Leu	Gln	Trp	Thr	Ala	Met	Ala	Leu	Pro	Ala	Leu	Ile	210	215	220	
Ser	Leu	Val	Ile	Gly	Phe	Ala	Phe	Gly	Ala	Leu	Tyr	Trp	Lys	Lys	Lys	225	230	235	240

Gln Ser Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu  
245 250 255

Asp Asn Glu Ile Ser Met Leu Gln Gln Lys Glu Arg Glu Phe Gln Glu  
260 265 270

Val

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu  
1 5 10 15

Leu Leu Phe Asn Pro Leu Val Lys Thr Lys Glu Ile Cys Gly Asn Pro  
20 25 30

Val Thr Asp Asn Val Lys Asp Ile Thr Lys Leu Val Ala Asn Leu Pro  
35 40 45

Asn Asp Tyr Met Ile Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu  
50 55 60

Pro Ser His Cys Trp Leu Arg Asp Met Val Ile Gln Leu Ser Leu Ser  
65 70 75 80

Leu Thr Thr Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser  
85 90 95

Asn Tyr Ser Ile Ile Asp Lys Leu Gly Lys Ile Val Asp Asp Leu Val  
100 105 110

Leu Cys Met Glu Glu Asn Ala Pro Lys Asn Ile Lys Glu Ser Pro Lys  
115 120 125

Arg Pro Glu Thr Arg Ser Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe  
130 135 140

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr  
145 150 155 160

Ser Asp Cys Val Leu Ser Ser Thr Leu Gly Pro Glu Lys Asp Ser Arg  
165 170 175

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser  
180 185 190



Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Ala Lys Ala Pro  
 195 200 205

Glu Asp Ser Gly Leu Gln Trp Thr Ala Met Ala Leu Pro Ala Leu Ile  
 210 215 220

Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Lys  
 225 230 235 240

Gln Ser Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu  
 245 250 255

Asp Asn Glu Ile Ser Met Leu Gln Gln Lys Glu Arg Glu Phe Gln Glu  
 260 265 270

Val

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Thr Trp Ile Ile Thr Cys Phe Cys Leu Gln Leu Leu Leu Leu Asn Pro  
 1 5 10 15

Leu Val Lys Ala Gln Ser Ser Cys Gly Asn Pro Val Thr Asp Asp Val  
 20 25 30

Asn Asp Ile Ala Lys Leu Val Gly Asn Leu Pro Asn Asp Tyr Leu Ile  
 35 40 45

Thr Leu Lys Tyr Val Pro Lys Met Asp Ser Leu Pro Asn His Cys Trp  
 50 55 60

Leu His Leu Met Val Pro Glu Phe Ser Arg Ser Leu His Asn Leu Leu  
 65 70 75 80

Gln Lys Phe Ser Asp Ile Ser Asp Met Ser Asp Val Leu Ser Asn Tyr  
 85 90 95

Ser Ile Ile Asn Asn Leu Thr Arg Ile Ile Asn Asp Leu Met Ala Cys  
 100 105 110

Leu Ala Phe Asp Lys Asn Lys Asp Phe Ile Lys Glu Asn Gly Leu His  
 115 120 125

Tyr Glu Glu Asp Arg Phe Ile Pro Glu Asn Phe Phe Arg Leu Phe Asn  
 130 135 140

Ser	Thr	Ile	Glu	Val	Tyr	Lys	Glu	Phe	Ala	Asp	Ser	Leu	Asp	Lys	Asn	145	150	155	160
Asp	Cys	Ile	Met	Pro	Ser	Thr	Val	Glu	Thr	Pro	Glu	Asn	Asp	Ser	Arg	165	170	175	
Val	Ala	Val	Thr	Lys	Thr	Ile	Ser	Phe	Pro	Pro	Val	Ala	Ala	Ser	Ser	180	185	190	
Leu	Arg	Asn	Asp	Ser	Ile	Gly	Ser	Asn	Thr	Ser	Ser	Asn	Ser	Asn	Lys	195	200	205	
Glu	Ala	Leu	Gly	Phe	Ile	Ser	Ser	Ser	Ser	Leu	Gln	Gly	Ile	Ser	Ile	210	215	220	
Ala	Leu	Thr	Ser	Leu	Leu	Ser	Leu	Leu	Ile	Gly	Phe	Ile	Leu	Gly	Ala	225	230	235	240
Ile	Tyr	Trp	Lys	Lys	Thr	His	Pro	Lys	Ser	Arg	Pro	Glu	Ser	Asn	Glu	245	250	255	
Thr	Ile	Gln	Cys	His	Gly	Cys	Gln	Glu	Glu	Asn	Glu	Ile	Ser	Met	Leu	260	265	270	
Gln	Gln	Lys	Glu	Lys	Glu	His	Leu	Gln	Val							275	280		

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Ile	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	1	5	10	15
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Gly	Ile	Cys	Arg	Asn	Arg	Val	20	25	30	
Thr	Asp	Val	Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	Lys	Asp	35	40	45	
Tyr	Met	Ile	Thr	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	Pro	Ser	50	55	60	
His	Cys	Trp	Ile	Ser	Glu	Met	Val	Glu	Gln	Leu	Ser	Val	Ser	Leu	Thr	65	70	75	80

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE:DNA

(A) NAME/KEY: CDS

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

48

GTT GTT GCT TCC GAA ACC TCC GAC TGC GTT GTT TCC TCC ACC CTG TCT	96
Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser	
20 25 30	
CCG GAA AAA GAC TCC CGT GTT TCG GTT ACC AAA CCG TTC ATG CTG CCG	144
Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro	
35 40 45	
CCG GTT GCT GCT TCC TCC CTG CGT AAC GAC TCC TCC TCC TCC AAC TCC	192
Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser	
50 55 60	
AAA TAC ATC TAC CTG ATC TAATAGGATC CG GTT ACC AAA CCG TTC ATG	240
Lys Tyr Ile Tyr Leu Ile Val Thr Lys Pro Phe Met	
65 70 75	
CTG CCG CCG GTT GCT GCT TAATAGGATC C	269
Leu Pro Pro Val Ala Ala	
80	

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe	
1 5 10 15	
Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser	
20 25 30	
Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro	
35 40 45	
Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser	
50 55 60	
Lys Tyr Ile Tyr Leu Ile Val Thr Lys Pro Phe Met Leu Pro Pro Val	
65 70 75 80	
Ala Ala	

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1404 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:DNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 184..1002

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 259..1002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCGCCTCGCG CCGAGACTAG AAGCGCTGCG GGAAGCAGGG ACAGTGGAGA GGGCGCTGCG	60
CTCGGGCTAC CCAATGCGTG GACTATCTGC CGCCGCTGTT CGTGCAATAT GCTGGAGCTC	120
CAGAACAGCT AAACGGAGTC GCCACACCAC TGTTTGTGCT GGATCGCAGC GCTGCCTTTC	180
CTT ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG	228
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln	
-25 -20 -15	
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG AAT	276
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn	
-10 -5 1 5	
CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA AAT CTT	324
Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu	
10 15 20	
CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG ATG GAT GTT	372
Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val	
25 30 35	
TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA CAA TTG TCA GAC	420
Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp	
40 45 50	
AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC TTG	468
Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu	
55 60 65 70	
AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG AAT ATA GTG GAT GAC CTT	516
Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu	
75 80 85	
GTG GAG TGC GTG AAA GAA AAC TCA TCT AAG GAT CTA AAA AAA TCA TTC	564
Val Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe	
90 95 100	
AAG AGC CCA GAA CCC AGG CTC TTT ACT CCT GAA GAA TTC TTT AGA ATT	612
Lys Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile	
105 110 115	

TTT AAT AGA TCC ATT GAT GCC TTC AAG GAC TTT GTA GTG GCA TCT GAA Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu 120 125 130	660
ACT AGT GAT TGT GTG GTT TCT TCA ACA TTA AGT CCT GAG AAA GAT TCC Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser 135 140 145 150	708
AGA GTC AGT GTC ACA AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC AGC Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser 155 160 165	756
TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT AGG AAG GCC AAA AAT CCC Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro 170 175 180	804
CCT GGA GAC TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG Pro Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu 185 190 195	852
TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys 200 205 210	900
AGA CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu 215 220 225 230	948
GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT CAA Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln 235 240 245	996
GAA GTG TAATTGTGGC TTGTATCAAC ACTGTTACTT TCGTACATTG GCTGGTAACA Glu Val	1052
GTTTCATGTTT GCTTCATAAA TGAAGCAGCT TTAAACAAAT TCATATTCTG TCTGGAGTGA	1112
CAGACCACAT CTTTATCTGT TCTTGCTACC CATGACTTTA TATGGATGAT TCAGAAATTG	1172
GAACAGAATG TTTTACTGTG AAAGTGGCAC TGAATTAATC ATCTATAAAG AAGAACTTGC	1232
ATGGAGCAGG ACTCTATTTT AAGGACTGCG GGAAGTGGGT CTCATTTAGA ACTTGCAGCT	1292
GATGTTGGAA GAGAAAGCAC GTGTCTCAGA CTGCATGTAC CATTTCATG GCTCCAGAAA	1352
TGTCTAAATG CTGAAAAAAC ACCTAGCTTT ATTCTTCAGA TACAACTGC AG	1404

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 273 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

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Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu
-25                      -20                      -15                      -10

Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg
                      -5                      1                      5

Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro
          10                      15                      20

Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu
          25                      30                      35

Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser
          40                      45                      50                      55

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
                      60                      65                      70

Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val
          75                      80                      85

Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys
          90                      95                      100

Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe
          105                      110                      115

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr
          120                      125                      130                      135

Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg
          140                      145                      150

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
          155                      160                      165

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro
          170                      175                      180

Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe
          185                      190                      195

Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg
          200                      205                      210                      215

Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu
          220                      225                      230

Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu
          235                      240                      245

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Val

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1088 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 151..885

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 226..885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AGCAGGGACA GTGGAGAGGG CGCTGCGCTC GGGCTACCCA ATGCGTGGAC TATCTGCCGC	60
CGCTGTTCGT GCAATATGCT GGAGCTCCAG AACAGCTAAA CGGAGTCGCC ACACCACTGT	120
TTGTGCTGGA TCGCAGCGCT GCCTTTCCTT ATG AAG AAG ACA CAA ACT TGG ATT	174
Met Lys Lys Thr Gln Thr Trp Ile	
-25 -20	
CTC ACT TGC ATT TAT CTT CAG CTG CTC CTA TTT AAT CCT CTC GTC AAA	222
Leu Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro Leu Val Lys	
-15 -10 -5	
ACT GAA GGG ATC TGC AGG AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC	270
Thr Glu Gly Ile Cys Arg Asn Arg Val Thr Asn Asn Val Lys Asp Val	
1 5 10 15	
ACT AAA TTG GTG GCA AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA	318
Thr Lys Leu Val Ala Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys	
20 25 30	
TAT GTC CCC GGG ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG	366
Tyr Val Pro Gly Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu	
35 40 45	
ATG GTA GTA CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT	414
Met Val Val Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe	
50 55 60	
TCA AAT ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT	462
Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu	
65 70 75	



GTG AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT	510
Val Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser	
80 85 90 95	
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT ACT	558
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe Thr	
100 105 110	
CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC TTC AAG	606
Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys	
115 120 125	
GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT TCT TCA ACA	654
Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr	
130 135 140	
TTA AGT CCT GAG AAA GGG AAG GCC AAA AAT CCC CCT GGA GAC TCC AGC	702
Leu Ser Pro Glu Lys Gly Lys Ala Lys Asn Pro Pro Gly Asp Ser Ser	
145 150 155	
CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG TTT TCT CTT ATA ATT	750
Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe Ser Leu Ile Ile	
160 165 170 175	
GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG AGA CAG CCA AGT CTT	798
Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg Gln Pro Ser Leu	
180 185 190	
ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA GAG GAT AAT GAG ATA	846
Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu Asp Asn Glu Ile	
195 200 205	
AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT CAA GAA GTG TAATTGTGGC	895
Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu Val	
210 215 220	
TTGTATCAAC ACTGTTACTT TCGTACATTG GCTGGTAACA GTTCATGTTT GCTTCATAAA	955
TGAAGCAGCT TTAAACAAAT TCATATTCTG TCTGGAGTGA CAGACCACAT CTTTATCTGT	1015
TCTTGCTACC CATGACTTTA TATGGATGAT TCAGAAATTG GAACAGAATG TTTTACTGTG	1075
AAACTGGCAC TGA	1088

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu  
 -25 -20 -15 -10

Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg  
 -5 1 5

Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro  
 10 15 20

Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu  
 25 30 35

Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser  
 40 45 50 55

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser  
 60 65 70

Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val  
 75 80 85

Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys  
 90 95 100

Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe  
 105 110 115

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr  
 120 125 130 135

Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Gly Lys Ala  
 140 145 150

Lys Asn Pro Pro Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu  
 155 160 165

Pro Ala Leu Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr  
 170 175 180

Trp Lys Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln  
 185 190 195

Ile Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg  
 200 205 210 215

Glu Phe Gln Glu Val  
 220

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Glu Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val Lys Asp Ile Thr  
1 5 10 15

Lys Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile Thr Leu Asn Tyr  
20 25 30

Val Ala Gly Met Asp Val Leu Pro Ser His Xaa Trp Leu Arg Asp  
35 40 45

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Ile Thr Thr Leu Asn Tyr Val Ala Gly Met  
1 5 10

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Xaa Xaa Leu Gly Pro  
1 5 10 15

Glu Lys Asp Ser Arg Val Ser Val Xaa Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Asp Val Leu Pro Ser His Cys Trp Leu Arg Asp Met  
1 5 10

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Glu Glu Asn Ala Pro Lys Asn Val Glu Ser Leu Lys Lys Pro Thr Arg  
1 5 10 15  
Asn Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe Asp Arg Ser Ile Asp  
20 25 30

Ala

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Glu Ser Leu Lys Lys Pro Glu Thr Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Val Ser Val Xaa Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ile	Val	Asp	Asp	Leu	Val	Ala	Ala	Met	Glu	Glu	Asn	Ala	Pro	Lys
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Asn	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Ser	Ile	Phe	Xaa	Arg
1				5					10			

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Leu	Val	Ala	Asn	Leu	Pro	Asn	Asp	Tyr	Met	Ile	Thr	Leu	Asn	Tyr	Val
1				5					10				15		

Ala	Gly	Asp	Asp	Val	Leu	Pro	Ser	His	Cys	Trp	Leu	Arg
				20				25				

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr Ser Asp  
1                      5                      10                      15

Cys Val Leu Ser Xaa Xaa Leu Gly  
20

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe  
1                      5                      10                      15

Phe Ser Ile Phe Xaa Arg  
20

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe  
1                      5                      10                      15

Phe Ser Ile Phe Asp Arg  
20

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Asn Ala Pro Lys Asn Val Lys Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ser Arg Val Ser Val Xaa Lys Pro Phe Met Leu Pro Pro Val Ala Ala  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe Phe  
1 5 10 15

Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala  
20 25 30

Ser Asp

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe Phe  
1 5 10 15

Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala  
20 25 30

Ser Asp Thr Ser Asp  
35

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Leu Arg Asp Met Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Leu  
1 5 10 15

Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile  
20 25 30

Asp Lys Leu Gly Lys Ile Val Asp  
35 40

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:



Pro Val Ala Ala

1

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CCTGAGAAAG ATTCCAGAGTC

21

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CTGCAGTTTG TATCTGAAG

19

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CATATAAAGT CATGGGTAG

19

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

ACTTGTGTCT TCTTCATAAG GAAAGGC

27

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TGTACGAAAG TAACAGTGTT G

21

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ACTGCTCCTA TTTAATCCTC TC

22

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CACTGACTCT GGAATCTTTC TCA

23

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TCGACCCGGA TCCCC

15

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TCGAGGGGAT CCGGG

15

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TCTTCTTCAT GGCGGCGGCA AGCTT

25

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp	Ser	Arg	Val	Ser	Val	Xaa	Lys	Pro	Phe	Phe	Met	Leu	Pro	Pro	Val
1				5				10					15		

Ala Ala

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Asp Ser Arg Val Ser Val Thr Lys Pro Phe Phe Met Leu Pro Pro Val  
1                      5                      10                      15  
  
Ala Ala

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CGATTTGATT CTAGAAGGAG GAATAACATA TGGTTAACGC GTTGAATTC GGTAC 55

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CGAATTCCAA CGCGTTAACC ATATGTTATT CCTCCTTCTA GAATCAAAT 49

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TATGCAGGA 9

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GATCTCCTGC A

11

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TATGGAAGGT ATCTGCA

17

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GATACCTTCC A

11

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTCCTTATG

10

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCCGCCGCCA TG

12

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TCTTCTTCAT GCGGCGGCA AGCTT

25